



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/892,287

DATE: 03/27/2003

TIME: 12:39:41

Input Set : A:\pf03342div_substitute sequence listing.txt

Output Set: N:\CRF4\03272003\I892287.raw

5-

1 <110> APPLICANT: Hillman, Jennifer L.; Lal, Preeti G.;

2 Corley, Neil C.; Shah, Purvi

4 <120> TITLE OF INVENTION: ANTIBODIES TO A HUMAN PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE

5 PHOSPHATASE (As amended)

7 <130> FILE REFERENCE: PF-0334-2 DIV

9 <140> CURRENT APPLICATION NUMBER: 09/892,287

10 <141> CURRENT FILING DATE: 2001-06-26

12 <150> PRIOR APPLICATION NUMBER: US 09/258,643

13 <151> PRIOR FILING DATE: 1999-02-26

15 <150> PRIOR APPLICATION NUMBER: US 08/884,681

16 <151> PRIOR FILING DATE: 1997-06-27

18 <160> NUMBER OF SEQ ID NOS: 5

19 <170> SOFTWARE: PERL Program

21 <210> SEQ ID NO: 1

22 <211> LENGTH: 372

23 <212> TYPE: PRT

24 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: misc_feature

28 <223> OTHER INFORMATION: Incyte ID No: 638789CD1

30 <400> SEQUENCE: 1

31	Met	Asp	Val	Leu	Ser	Pro	Leu	Ser	Phe	Ile	Lys	Val	Ser	His	Val
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33	Arg	Met	Gln	Gly	Ile	Leu	Leu	Leu	Val	Phe	Ala	Lys	Tyr	Gln	His
34					20					25					30
35	Leu	Pro	Tyr	Ile	Gln	Ile	Leu	Ser	Thr	Lys	Ser	Thr	Pro	Thr	Gly
36					35					40					45
37	Leu	Phe	Gly	Tyr	Trp	Gly	Asn	Lys	Gly	Gly	Val	Asn	Ile	Cys	Leu
38					50					55					60
39	Lys	Leu	Tyr	Gly	Tyr	Tyr	Val	Ser	Ile	Ile	Asn	Cys	His	Leu	Pro
40					65					70					75
41	Pro	His	Ile	Ser	Asn	Asn	Tyr	Gln	Arg	Leu	Glu	His	Phe	Asp	Arg
42					80					85					90
43	Ile	Leu	Glu	Met	Gln	Asn	Cys	Glu	Gly	Arg	Asp	Ile	Pro	Asn	Ile
44					95					100					105
45	Leu	Asp	His	Asp	Leu	Ile	Ile	Trp	Phe	Gly	Asp	Met	Asn	Phe	Arg
46					110					115					120
47	Ile	Glu	Asp	Phe	Gly	Leu	His	Phe	Val	Arg	Glu	Ser	Ile	Lys	Asn
48					125					130					135
49	Arg	Cys	Tyr	Gly	Gly	Leu	Trp	Glu	Lys	Asp	Gln	Leu	Ser	Ile	Ala
50					140					145					150
51	Lys	Lys	His	Asp	Pro	Leu	Leu	Arg	Glu	Phe	Gln	Glu	Gly	Arg	Leu
52					155					160					165

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53 Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn Ser Asn Asp Tyr
54                               170                     175                     180
55 Asp Thr Ser Glu Lys Lys Arg Lys Pro Ala Trp Thr Asp Arg Ile
56                               185                     190                     195
57 Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp Thr Pro
58                               200                     205                     210
59 Ile Pro Pro Ala Ser His Phe Ser Leu Ser Leu Arg Gly Tyr Ser
60                               215                     220                     225
61 Ser His Met Thr Tyr Gly Ile Ser Asp His Lys Pro Val Ser Gly
62                               230                     235                     240
63 Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser Ala Pro Leu Ile
64                               245                     250                     255
65 Val Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn Asp Met Met
66                               260                     265                     270
67 Val Ser Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro Trp Asp
68                               275                     280                     285
69 Trp Ile Gly Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp Tyr
70                               290                     295                     300
71 Val Ser Tyr Ala Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp
72                               305                     310                     315
73 Asn Leu Asn Gln Val Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr
74                               320                     325                     330
75 Glu Asp Glu Phe Leu Leu Cys Tyr Tyr Ser Asn Ser Leu Arg Ser
76                               335                     340                     345
77 Val Val Gly Ile Ser Arg Pro Phe Gln Ile Pro Pro Gly Ser Leu
78                               350                     355                     360
79 Arg Glu Asp Pro Leu Gly Glu Ala Gln Pro Gln Ile
80                               365                     370

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82 <210> SEQ ID NO: 2

83 <211> LENGTH: 2573

84 <212> TYPE: DNA

85 <213> ORGANISM: Homo sapiens

87 <220> FEATURE:

88 <221> NAME/KEY: misc feature

89 <223> OTHER INFORMATION: Incyte ID No: 638789CB1

91 <400> SEQUENCE: 2

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93 cagtgacctg cttcagctga acaaccggaa cctcaatctt gacatatatg ttattggttt 120
94 gcaggaattg aactctggga tcataagcct cctttccgat gctgccttta atgactcgtg 180
95 gagcagtttc ctcatggatg tgctttcccc tctgagcttc atcaaggtct cccatgtccg 240
96 tatgcagggg atcctcttac tggcttttgc caagtatcag catttgccct atatccagat 300
97 tctgtctact aaatccaccc ccactggcct gtttgggtac tgggggaaca aaggtggagt 360
98 caacatctgc ctgaagcttt atggctacta tgtcagcatc atcaactgcc acctgcctcc 420
99 ccacatttcc aacaattacc agcggctgga gcactttgac cggatcctgg agatgcagaa 480
100 ttgtgagggg cgagacatcc caaacatcct ggaccacgac ctcattatct ggtttggaga 540
101 catgaacttt cggatcgagg actttgggtt gcactttgtt cggaatcca ttaaaaatcg 600
102 gtgctacggt ggctgtggg agaaggacca gctcagcatt gccaagaaac atgacccgct 660
103 gctccgggag ttccaggagg gccgcctact cttcccgcc acctacaagt ttgataggaa 720
104 ctccaacgac tatgacacca gtgagaaaaa acgcaagcct gcatggaccg atcgcatcct 780

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105 gtggaggctg aagcggcagc cctgtgctgg ccccgacact cccataccgc cggcgtcaca 840
106 cttctccttg tctctgaggg gctacagcag ccacatgacg tacggcatca gcgaccacaa 900
107 gcctgtctcc ggcacgttcg acttgagct gaagccattg gtgtctgctc cgctgatcgt 960
108 cctgatgccc gaggacctgt ggaccgtgga aaatgacatg atggtcagct actcttcaac 1020
109 ctcggaacttc cccagcagcc cgtgggactg gattggactg tacaagggtg ggctgcggga 1080
110 cgттаатгac tacgtgtcct atgcctgggt cggggacagc aaggtctcct gcagcgacaa 1140
111 cctgaaccag gtttacatcg acatcagcaa tatccctacc actgaagatg agtttctcct 1200
112 ctgttactac agcaacagtc tgcgttctgt ggtggggata agcagaccct tccagatccc 1260
113 gcctggctcc ttgagggagg acccactggg tgaagcacag ccacagatct gagccaggat 1320
114 gggagtgaat cccaggcggg ggccagagct ggcagccagc tctgccttcc cactgcgggg 1380
115 agtgctgggg gccagccctg gcccctgaa gagacagcca agtgctgctc acatactcct 1440
116 cccagagtga gctctaacca ggctcatttg ctctctccac tactcatctc tggaattagc 1500
117 cgcttaaata cagggtttttg ttgctgagat gtgagtgaag ccagctagtg tgtcaacagt 1560
118 gaagacctgg ggacagttct gcgtctcatt tctggattcc taccctctct tctagtcttg 1620
119 cccaagtagt cctgccaggc acatgcccc a tttggcacag gcctgcattc ttgtcgtgcc 1680
120 gtcctggggc tcaggctgtc tgggagggga gatgctcaca tttgtacagg ctacatagac 1740
121 tggtgcaagc agtgctggat tccaggagtc ttggcatctc atagcttgct cccgtgagga 1800
122 gtgagcagag ggtctgggat ttctgcttcc agcaaaagca gtctgactca gtgggcagaa 1860
123 tggagggggc cctctagcca ggctcttacg ccattggtat gagcagggtg atgagggtcc 1920
124 ttcgggccagc acaaccttcc tccctactca cggcatggag tctgactgca tggaagtcc 1980
125 agatcctgac agagagaact gggaaggatc cagggttcgct tccgttggtg gcttgagtcc 2040
126 catgcctcca cctgccatc tgaggaaggg gtgacaagtg gtcaaggagc tgtggccaca 2100
127 gacttttcca ggggtgtcct tggcaggtag ggtgcgtctg tgccaccctt gtcaggagtc 2160
128 attgacgacg ggccccccct ggaccccccg ggacctcaga gtgggggcag gcagaaggga 2220
129 gaaccagctc aagacatttt ggaggatctg gccctggggg tcttcagaga acaccctcta 2280
130 ggggcttttg ggacatggcc tgtccccaca tccagcactt gcctccgcca tggctactcg 2340
131 gcagcccttt tcccaggaga agacacctct gggagcctgc tcagtgttg tccctgccatc 2400
132 ctgtgtcctg ggactgaggg ttactccagt tgctctgtgt tgcatactct cccccgcaag 2460
133 cctgtgtatg aagaattgtc ccctggcttc cagcaggcca tggctggctg ttttgtgact 2520
134 gttacattgt gcaggggtaa ttattagcgt ggcttttaca cttaaaaaaa aaa 2573

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136 <210> SEQ ID NO: 3

137 <211> LENGTH: 397

138 <212> TYPE: PRT

139 <213> ORGANISM: Homo sapiens

141 <220> FEATURE:

142 <221> NAME/KEY: misc_feature

143 <223> OTHER INFORMATION: GenBank ID No: g1399105

145 <400> SEQUENCE: 3

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146 Ala Arg Gly Leu His Phe Val Lys Phe Ala Ile Asp Ser Asp Gln
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148 Leu His Gln Leu Trp Glu Lys Asp Gln Leu Asn Met Ala Lys Asn
149                      20                      25                      30
150 Thr Trp Pro Ile Leu Lys Gly Phe Gln Glu Gly Pro Leu Asn Phe
151                      35                      40                      45
152 Ala Pro Thr Phe Lys Phe Asp Val Gly Thr Asn Lys Tyr Asp Thr
153                      50                      55                      60
154 Ser Ala Lys Lys Arg Lys Pro Ala Trp Thr Asp Arg Ile Leu Trp
155                      65                      70                      75
156 Lys Val Lys Ala Pro Gly Gly Gly Pro Ser Pro Ser Gly Arg Lys

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157		80		85		90
158	Ser His Arg Leu Gln Val Thr Gln His Ser Tyr Arg Ser His Met					
159		95		100		105
160	Glu Tyr Thr Val Ser Asp His Lys Pro Val Ala Ala Gln Phe Leu					
161		110		115		120
162	Leu Gln Phe Ala Phe Arg Asp Asp Met Pro Leu Val Arg Leu Glu					
163		125		130		135
164	Val Ala Asp Glu Trp Val Arg Pro Glu Gln Ala Val Val Arg Tyr					
165		140		145		150
166	Arg Met Glu Thr Val Phe Ala Arg Ser Ser Trp Asp Trp Ile Gly					
167		155		160		165
168	Leu Tyr Arg Val Gly Phe Arg His Cys Lys Asp Tyr Val Ala Tyr					
169		170		175		180
170	Val Trp Ala Lys His Glu Asp Val Asp Gly Asn Thr Tyr Gln Val					
171		185		190		195
172	Thr Phe Ser Glu Glu Ser Leu Pro Lys Gly His Gly Asp Phe Ile					
173		200		205		210
174	Leu Gly Tyr Tyr Ser His Asn His Ser Ile Leu Ile Gly Ile Thr					
175		215		220		225
176	Glu Pro Phe Gln Ile Ser Leu Pro Ser Ser Glu Leu Ala Ser Ser					
177		230		235		240
178	Ser Thr Asp Ser Ser Gly Thr Ser Ser Glu Gly Glu Asp Asp Ser					
179		245		250		255
180	Thr Leu Glu Leu Leu Ala Pro Lys Ser Arg Ser Pro Ser Pro Gly					
181		260		265		270
182	Lys Ser Lys Arg His Arg Ser Arg Ser Pro Gly Leu Ala Arg Phe					
183		275		280		285
184	Pro Gly Leu Ala Leu Arg Pro Ser Ser Arg Glu Arg Arg Gly Ala					
185		290		295		300
186	Ser Arg Ser Pro Ser Pro Gln Ser Arg Arg Leu Ser Arg Val Ala					
187		305		310		315
188	Pro Asp Arg Ser Ser Asn Gly Ser Ser Arg Gly Ser Ser Glu Glu					
189		320		325		330
190	Gly Pro Ser Gly Leu Pro Gly Pro Trp Ala Phe Pro Pro Ala Val					
191		335		340		345
192	Pro Arg Ser Leu Gly Leu Leu Pro Ala Leu Arg Leu Glu Thr Val					
193		350		355		360
194	Asp Pro Gly Gly Gly Gly Ser Trp Gly Pro Asp Arg Glu Ala Leu					
195		365		370		375
196	Ala Pro Asn Ser Leu Ser Pro Ser Pro Gln Gly His Arg Gly Leu					
197		380		385		390
198	Glu Glu Gly Gly Leu Gly Pro					
199		395				
201	<210> SEQ ID NO: 4					
202	<211> LENGTH: 942					
203	<212> TYPE: PRT					
204	<213> ORGANISM: Homo sapiens					
206	<220> FEATURE:					
207	<221> NAME/KEY: misc_feature					

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208 <223> OTHER INFORMATION: GenBank ID No: g1019103

210 <400> SEQUENCE: 4

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211 Val Thr Val Pro Glu Pro Gly Ala Ala Glu Ser Arg Ala Pro Cys
212   1           5           10           15
213 Gly Asp Ser Ser Gly Gly Cys Val Arg Ser Ala Gly Ala Ser Met
214           20           25           30
215 Asp Gln Ser Val Ala Ile Gln Glu Thr Leu Ala Glu Gly Glu Tyr
216           35           40           45
217 Cys Val Ile Ala Val Gln Gly Val Leu Cys Glu Gly Asp Ser Arg
218           50           55           60
219 Gln Ser Arg Leu Leu Gly Leu Val Arg Tyr Arg Leu Glu His Gly
220           65           70           75
221 Gly Gln Glu His Ala Leu Phe Leu Tyr Thr His Arg Arg Met Ala
222           80           85           90
223 Ile Thr Gly Asp Asp Val Ser Leu Asp Gln Ile Val Pro Val Ser
224           95          100          105
225 Arg Asp Phe Thr Leu Glu Glu Val Ser Pro Asp Gly Glu Leu Tyr
226          110          115          120
227 Ile Leu Gly Ser Asp Val Thr Val Gln Leu Asp Thr Ala Glu Leu
228          125          130          135
229 Ser Leu Val Phe Gln Leu Pro Phe Gly Ser Gln Thr Arg Met Phe
230          140          145          150
231 Leu His Glu Val Ala Arg Ala Cys Pro Gly Phe Asp Ser Ala Thr
232          155          160          165
233 Arg Asp Pro Glu Phe Leu Trp Leu Ser Arg Tyr Arg Cys Ala Glu
234          170          175          180
235 Leu Glu Leu Glu Met Pro Thr Pro Arg Gly Cys Asn Ser Ala Leu
236          185          190          195
237 Val Thr Trp Pro Gly Tyr Ala Thr Ile Gly Gly Gly Gly Ser Asn
238          200          205          210
239 Phe Asp Gly Leu Arg Pro Asn Gly Lys Gly Val Pro Met Asp Gln
240          215          220          225
241 Ser Ser Arg Gly Gln Asp Lys Pro Glu Ser Leu Gln Pro Arg Gln
242          230          235          240
243 Asn Lys Ser Lys Ser Glu Ile Thr Asp Met Val Arg Ser Ser Thr
244          245          250          255
245 Ile Thr Val Ser Asp Lys Ala His Ile Leu Ser Met Gln Lys Phe
246          260          265          270
247 Gly Leu Arg Asp Thr Ile Val Lys Ser His Leu Leu Gln Lys Glu
248          275          280          285
249 Glu Asp Tyr Thr Tyr Ile Gln Asn Phe Arg Phe Phe Ala Gly Thr
250          290          295          300
251 Tyr Asn Val Asn Gly Gln Ser Pro Lys Glu Cys Leu Arg Leu Trp
252          305          310          315
253 Leu Ser Asn Gly Ile Gln Ala Pro Asp Val Tyr Cys Val Gly Phe
254          320          325          330
255 Gln Glu Leu Asp Leu Ser Lys Glu Ala Phe Phe Phe His Asp Thr
256          335          340          345
257 Pro Lys Glu Glu Glu Trp Phe Lys Ala Val Ser Glu Gly Leu His

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VERIFICATION SUMMARY

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